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      RESULT 11
      XXXX HELLO
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      130394
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      01 FEB 1991
      (Rel. 17, "stated
      (Rel. 17, "last sequence
      STANDARD;
      PRT;
      19.04
  
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SQ Sequence 27 AA, 100.0% Score 132, DB 21, Length 27
Query Match 100.0%, Pos: No. 3,86-42,
Best Local Similarity 100.0%; Pwd: No. 3,86-42,
Matches 27, Conservative 0, Mismatches 0, Gaps 0, Gap
CY 1 HSDGFTSELSPLREAPRLPGLQGV 27
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 HSDGFTSELSPLREAPRLPGLQGV 27

RESULT 4
AAB70890 AAB70890 standard; peptide; 27 AA.
AAE70890;
XX
XX AAE70890;
XX
XX 26-JUN-2001 (first entry)
XX
XX Human secretin peptide.
XX
XX Seretlin; human, nociferic acid, treatment, prevention
XX Homo sapiens.
XX
XX W0200132196-A1.
XX
XX PD 10-MAY-2001.
XX
XX PF 03-NOV-2000; Z600W-EPI0847.
XX
XX PR 05-NOV-1999; 99DE-1053339.
XX
XX RA (GOLD-) GOLDHAM PHARMA GmbH.
XX
XX RI Frank A., Jordan K., Hebel W.
XX
XX WP1: 2001-000000000e
XX
XX XX Pharmacological composition for preventing treatment of autism
XX containing this peptide fragment having 4-15 (preferably 4-9) amino
XX acids (originally in this addition said first and which have certain
XX activity. The peptide fragments described in the invention (of any
XX origin, e.g. derived from human, porcine, chicken or other species)
XX have a specific beneficial action in the treatment or prevention of
XX autism. They are free of the other activities (e.g. gastrointestinal
XX effects) of secretin itself. This sequence represents the human secretin
XX peptide used to generate the peptide fragments described in the method
XX of the invention.
SQ Sequence 27 AA;
Query Match 100.0%; Score 132, DB 21, Length 27,
Best Local Similarity 100.0%; Pwd: No. 3,86-42,
Matches 27, Conservative 0, Mismatches 0, Gaps 0, Gap
CY 1 HSDGFTSELSPLREAPRLPGLQGV 27
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 HSDGFTSELSPLREAPRLPGLQGV 27

RESULT 5
AAB91261 AAB91261 standard; Peptide; 27 AA.
XX
XX AC AAB91261;
XX
```

[illegible]

[illegible][illegible]

PN W02002:16195 A:

[illegible]

**A**

1. **Introduction**  
 2. **Background**  
 3. **Methodology**  
 4. **Results**  
 5. **Conclusion**  
 6. **References**

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[illegible]

Am. J. Hyg.

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**Abstract**





P1 Tsuji M, Hataake Y, Koiwa A;  
 XX  
 DP WPI: 1993-24132E/13 (24132E).  
 XX  
 PT Hepatic secretion of secretin for high yield purification of high  
 XX  
 PS purity secretin on strong acid treatment  
 XX  
 PS Claim 1; Page 43; 47pp; English.

XX The sequence in AAP0039 is a precursor for the production of  
 CC secretin. The peptide sequences given in AAP0039 are the pre-  
 CC secretin which are useful in the production of this precursor. The precursor is  
 CC treated with strong acid in the preparation of secretin. Secretin is  
 CC one of the digestive tract hormones and is useful in the treatment of  
 CC pancreatic external secretion, controlling gastric-stimulating secretion  
 CC of the stomach acid, releasing insulin, stimulating secretion of peptide  
 CC and decomposing fat. It is used as a pancreatic-function examining  
 CC agent and a medicine for curing duodenal ulcers etc.  
 XX  
 SQ Sequence 27 AA;

Query Match 93.2% Score 123; DP 4; Length 27;  
 Best Local Similarity 92.6% Pred. No. 7.6e-11;  
 Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HSDGFTSELSRPSRAGAPLQPLQGV 27  
 1 HSDGFTSELSRPSRAGAPLQPLQGV 27

RESULT 13  
 AAP0021  
 ID AAP0003 standard; peptide; 27 AA

XX AAP0021;

XX 03-SEP-1992 (first entry)

XX Synthetic secretion

XX Pharmacologically: hypersecretion, hypersecretion, hypersecretion,  
 XX duodenal ulcer.

XX Synthetic

XX JPS814435-A.

XX 27-ATG-1981.

XX 22-FEB-1992; 927P-0007000

XX 22-FEB-1992; 927P-0007000

XX (EISA) EISA KK.

XX WPI: 1993-779933/40.

XX Pharmacologically active secretin (purity) by removing inhibition

XX gp. from hepatic secretin

XX Claim 1; Page 2; 13pp; Japanese.

XX Secretin, which has been purified by various methods from  
 CC porcine duodenum, may be produced by standard solid phase synthesis.

CC Secretin is a digestive tract hormone with many useful

CC pharmacological actions such as pancreatic secretion promotion,  
 CC gastric stimulation, gastric acid secretion inhibition, insulin

CC release, stimulation of peptide secretion and lipolytic action. It  
 CC is useful as a reagent for test of pancreatic function and as a remedy for  
 CC duodenal ulcers.  
 XX  
 XX Sequence 27 AA;

Query Match 93.2% Score 123; DP 4; Length 27;  
 Best Local Similarity 92.6% Pred. No. 7.6e-11;  
 Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HSDGFTSELSRPSRAGAPLQPLQGV 27  
 1 HSDGFTSELSRPSRAGAPLQPLQGV 27

RESULT 14  
 AAP0014  
 ID AAP0014 standard; peptide; 27 AA

XX AAP0014;

XX 03-SEP-1992 (first entry)

XX 03-SEP-1992 (first entry)

XX Diagnostic, duodenal ulcer; pancreas.

XX Synthetic

XX JPS7200343-A.

XX 08-DEC-1992.

XX 02-JUN-1981; 91JP-0084603.

XX 02-JUN-1981; 91JP-0084603.

XX 01-JAN-1981; 81JP-0106607.

XX 04-FEB-1982; 82JP-0016734.

XX 02-JUN-1981; 81JP-0084604.

XX (EISA) EISA KK.

XX WPI: 1993-080562/04 (080562).

XX 27 Dec amino secretin (purity) by recombinant DNA technique

XX useful as diagnostic agent for pancreatic function or that of

XX (purity) 1; 4pp; 27 pp

XX Claim 1; Page 1; 15pp; Japanese.

XX Production of the peptide comprises chemical synthesis of the peptide  
 CC expression gene, introduction of the gene into a plasmid vector,  
 CC growing in a host microorganism, thereby giving a culture supernatant  
 CC which can grow in the microorganism, transformation of the host cell  
 CC by the plasmid and cultivation of the resultant transformant and  
 CC recovery of the peptide. The peptide is useful as a diagnostic  
 CC agent for pancreatic function or as a drug for treatment of duodenal  
 CC ulcer. The peptide is purified by a method of liquid chromatography in  
 CC good yield on large scale with low cost.

XX Sequence 27 AA;

Query Match 93.2% Score 123; DP 4; Length 27;  
 Best Local Similarity 92.6% Pred. No. 7.6e-11;  
 Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HSDGFTSELSRPSRAGAPLQPLQGV 27  
 1 HSDGFTSELSRPSRAGAPLQPLQGV 27

RESULT 15

AAP0038

XX AAP0038;

XX 04-SEP-1992 (first entry)

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GenCore version 5.1.4.P5.4579  
Copyright (c) 1993 - 2003 Compugen Ltd

## OM protein - protein search, using sw model

Run on: May 27, 2003, 18:01:32, Search time: 14 seconds  
(without alignments)  
56,744 Million cell updates/sec

Title: US-09-897-412-10

Perfect score: 132

Sequence: 1 HSDGTFPSRLSPFPSPAPICPILQGV 27

Scoring table:

BLOSUM62  
Gap: 10.0, Gapext: 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match: 0%

Maximum Match: 100%

Listing first 45 summaries:

## Database:

Issued Patents, AA\*  
1: /cgn2\_6/pdatat1/134/5A\_GOWB\_FEG\*  
2: /cgn2\_6/pdatat1/134/5B\_GOWB\_FEG\*  
3: /cgn2\_6/pdatat1/134/6A\_GOWB\_FEG\*  
4: /cgn2\_6/pdatat1/134/6B\_GOWB\_FEG\*  
5: /cgn2\_6/pdatat1/134/6C\_GOWB\_FEG\*  
6: /cgn2\_6/pdatat1/134/6D\_GOWB\_FEG\*

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	132	100.0	27	1	US-07-924-054-10
2	132	100.0	27	1	US-08-062-472B-43
3	123	92.2	27	1	US-08-010-100-6
4	123	92.2	27	2	US-08-010-002-36
5	123	92.2	27	4	US-08-010-002-36
6	123	92.2	27	4	US-08-010-002-36
7	123	92.2	27	4	US-08-010-002-36
8	123	92.2	27	4	US-08-010-002-36
9	123	92.2	27	4	US-08-010-002-36
10	123	92.2	27	4	US-08-010-002-36
11	108.5	82.0	26	1	US-07-924-054-10
12	60	47.0	31	4	US-09-333-415-11
13	61	46.2	32	4	US-09-333-415-11
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15	61	46.2	32	4	US-09-333-415-11
16	61	46.2	32	4	US-09-333-415-11
17	61	46.2	32	4	US-09-333-415-11
18	61	46.2	32	4	US-09-333-415-11
19	61	46.2	32	4	US-09-333-415-11
20	60	45.5	31	4	US-09-333-415-11
21	60	45.5	31	4	US-09-333-415-11
22	60	45.5	31	4	US-09-333-415-11
23	60	45.5	31	4	US-09-333-415-11
24	60	45.5	31	4	US-09-333-415-11
25	60	45.5	31	4	US-09-333-415-11
26	60	45.5	31	4	US-09-333-415-11
27	60	45.5	31	4	US-09-333-415-11

28	60	45.5	40	4	US-09-623-618B-34	Sequence 14, Appl
29	59	44.7	29	1	US-07-741-931-2	Sequence 17, Appl
30	59	44.7	29	1	US-08-066-480-7	Sequence 17, Appl
31	59	44.7	29	1	US-08-066-480-7	Sequence 17, Appl
32	59	44.7	29	1	US-08-066-480-7	Sequence 17, Appl
33	59	44.7	29	1	US-08-066-480-7	Sequence 17, Appl
34	59	44.7	29	1	US-08-066-480-7	Sequence 17, Appl
35	59	44.7	29	1	US-08-066-480-7	Sequence 17, Appl
36	59	44.7	29	1	US-08-066-480-7	Sequence 17, Appl
37	59	44.7	29	1	US-08-066-480-7	Sequence 17, Appl
38	59	44.7	29	1	US-08-066-480-7	Sequence 17, Appl
39	59	44.7	29	1	US-08-066-480-7	Sequence 17, Appl
40	59	44.7	29	1	US-08-066-480-7	Sequence 17, Appl
41	59	44.7	29	1	US-08-066-480-7	Sequence 17, Appl
42	59	44.7	29	1	US-08-066-480-7	Sequence 17, Appl
43	59	44.7	29	1	US-08-066-480-7	Sequence 17, Appl
44	59	44.7	29	1	US-08-066-480-7	Sequence 17, Appl
45	59	44.7	29	1	US-08-066-480-7	Sequence 17, Appl

## ALIGNMENTS

RESULT 1  
US-07-924-054-10  
Sequence 10, Application us/07924054  
Patent No. 5486472  
GENERAL INFORMATION:  
APPLICANT: SUZUKI, NO. 5486472united  
APPLICANT: KITADA, CHIEKO  
INVENTOR: KITADA, CHIEKO  
TITLE: INVENTION, METHOD FOR PRODUCING AND USE THEREOF  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESS: 130 Water Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: WINDOWS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.05  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07924054  
FILING DATE: 19990603  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: FISHBEIN, DAVID S.  
REGISTRATION NUMBER: 31254  
FIRM/INSTITUTION INFORMATION:  
FIRM/INSTITUTION INFORMATION: 40805  
TELEPHONE: 617-552-3170  
TELEFAX: 617-552-3170  
TELEX: 312543 312543  
INVENTOR: KITADA, CHIEKO  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULAR TYPE: protein  
DB ID: 07-924-054-10  
Query Match: 100.0, Query Length: 27, DB ID: 07-924-054-10  
Best Local Similarity: 100.0, Query Length: 27, DB ID: 07-924-054-10  
Matches: 27, Conserved: 27, Mismatches: 0, Indels: 0  
1 HSDGTFPSRLSPFPSPAPICPILQGV 27  
1 HSDGTFPSRLSPFPSPAPICPILQGV 27



```

; SEQ ID NO 52
; LENGTH: 27

```

Figure 1. The effect of the concentration of the *Agrobacterium* suspension on the transformation efficiency of *Agrobacterium* strains. The *Agrobacterium* strains were grown in the YEA medium for 24 h and then adjusted to the OD<sub>600</sub> of 0.1. The *Agrobacterium* strains were then grown in the YEA medium with the concentration of 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2.0, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3.0, 3.1, 3.2, 3.3, 3.4, 3.5, 3.6, 3.7, 3.8, 3.9, 4.0, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5.0, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6.0, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7.0, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9, 8.0, 8.1, 8.2, 8.3, 8.4, 8.5, 8.6, 8.7, 8.8, 8.9, 9.0, 9.1, 9.2, 9.3, 9.4, 9.5, 9.6, 9.7, 9.8, 9.9, 10.0, 10.1, 10.2, 10.3, 10.4, 10.5, 10.6, 10.7, 10.8, 10.9, 11.0, 11.1, 11.2, 11.3, 11.4, 11.5, 11.6, 11.7, 11.8, 11.9, 12.0, 12.1, 12.2, 12.3, 12.4, 12.5, 12.6, 12.7, 12.8, 12.9, 13.0, 13.1, 13.2, 13.3, 13.4, 13.5, 13.6, 13.7, 13.8, 13.9, 14.0, 14.1, 14.2, 14.3, 14.4, 14.5, 14.6, 14.7, 14.8, 14.9, 15.0, 15.1, 15.2, 15.3, 15.4, 15.5, 15.6, 15.7, 15.8, 15.9, 16.0, 16.1, 16.2, 16.3, 16.4, 16.5, 16.6, 16.7, 16.8, 16.9, 17.0, 17.1, 17.2, 17.3, 17.4, 17.5, 17.6, 17.7, 17.8, 17.9, 18.0, 18.1, 18.2, 18.3, 18.4, 18.5, 18.6, 18.7, 18.8, 18.9, 19.0, 19.1, 19.2, 19.3, 19.4, 19.5, 19.6, 19.7, 19.8, 19.9, 20.0, 20.1, 20.2, 20.3, 20.4, 20.5, 20.6, 20.7, 20.8, 20.9, 21.0, 21.1, 21.2, 21.3, 21.4, 21.5, 21.6, 21.7, 21.8, 21.9, 22.0, 22.1, 22.2, 22.3, 22.4, 22.5, 22.6, 22.7, 22.8, 22.9, 23.0, 23.1, 23.2, 23.3, 23.4, 23.5, 23.6, 23.7, 23.8, 23.9, 24.0, 24.1, 24.2, 24.3, 24.4, 24.5, 24.6, 24.7, 24.8, 24.9, 25.0, 25.1, 25.2, 25.3, 25.4, 25.5, 25.6, 25.7, 25.8, 25.9, 26.0, 26.1, 26.2, 26.3, 26.4, 26.5, 26.6, 26.7, 26.8, 26.9, 27.0, 27.1, 27.2, 27.3, 27.4, 27.5, 27.6, 27.7, 27.8, 27.9, 28.0, 28.1, 28.2, 28.3, 28.4, 28.5, 28.6, 28.7, 28.8, 28.9, 29.0, 29.1, 29.2, 29.3, 29.4, 29.5, 29.6, 29.7, 29.8, 29.9, 30.0, 30.1, 30.2, 30.3, 30.4, 30.5, 30.6, 30.7, 30.8, 30.9, 31.0, 31.1, 31.2, 31.3, 31.4, 31.5, 31.6, 31.7, 31.8, 31.9, 32.0, 32.1, 32.2, 32.3, 32.4, 32.5, 32.6, 32.7, 32.8, 32.9, 33.0, 33.1, 33.2, 33.3, 33.4, 33.5, 33.6, 33.7, 33.8, 33.9, 34.0, 34.1, 34.2, 34.3, 34.4, 34.5, 34.6, 34.7, 34.8, 34.9, 35.0, 35.1, 35.2, 35.3, 35.4, 35.5, 35.6, 35.7, 35.8, 35.9, 36.0, 36.1, 36.2, 36.3, 36.4, 36.5, 36.6, 36.7, 36.8, 36.9, 37.0, 37.1, 37.2, 37.3, 37.4, 37.5, 37.6, 37.7, 37.8, 37.9, 38.0, 38.1, 38.2, 38.3, 38.4, 38.5, 38.6, 38.7, 38.8, 38.9, 39.0, 39.1, 39.2, 39.3, 39.4, 39.5, 39.6, 39.7, 39.8, 39.9, 40.0, 40.1, 40.2, 40.3, 40.4, 40.5, 40.6, 40.7, 40.8, 40.9, 41.0, 41.1, 41.2, 41.3, 41.4, 41.5, 41.6, 41.7, 41.8, 41.9, 42.0, 42.1, 42.2, 42.3, 42.4, 42.5, 42.6, 42.7, 42.8, 42.9, 43.0, 43.1, 43.2, 43.3, 43.4, 43.5, 43.6, 43.7, 43.8, 43.9, 44.0, 44.1, 44.2, 44.3, 44.4, 44.5, 44.6, 44.7, 44.8, 44.9, 45.0, 45.1, 45.2, 45.3, 45.4, 45.5, 45.6, 45.7, 45.8, 45.9, 46.0, 46.1, 46.2, 46.3, 46.4, 46.5, 46.6, 46.7, 46.8, 46.9, 47.0, 47.1, 47.2, 47.3, 47.4, 47.5, 47.6, 47.7, 47.8, 47.9, 48.0, 48.1, 48.2, 48.3, 48.4, 48.5, 48.6, 48.7, 48.8, 48.9, 49.0, 49.1, 49.2, 49.3, 49.4, 49.5, 49.6, 49.7, 49.8, 49.9, 50.0, 50.1, 50.2, 50.3, 50.4, 50.5, 50.6, 50.7, 50.8, 50.9, 51.0, 51.1, 51.2, 51.3, 51.4, 51.5, 51.6, 51.7, 51.8, 51.9, 52.0, 52.1, 52.2, 52.3, 52.4, 52.5, 52.6, 52.7, 52.8, 52.9, 53.0, 53.1, 53.2, 53.3, 53.4, 53.5, 53.6, 53.7, 53.8, 53.9, 54.0, 54.1, 54.2, 54.3, 54.4, 54.5, 54.6, 54.7, 54.8, 54.9, 55.0, 55.1, 55.2, 55.3, 55.4, 55.5, 55.6, 55.7, 55.8, 55.9, 56.0, 56.1, 56.2, 56.3, 56.4, 56.5, 56.6, 56.7, 56.8, 56.9, 57.0, 57.1, 57.2, 57.3, 57.4, 57.5, 57.6, 57.7, 57.8, 57.9, 58.0, 58.1, 58.2, 58.3, 58.4, 58.5, 58.6, 58.7, 58.8, 58.9, 59.0, 59.1, 59.2, 59.3, 59.4, 59.5, 59.6, 59.7, 59.8, 59.9, 60.0, 60.1, 60.2, 60.3, 60.4, 60.5, 60.6, 60.7, 60.8, 60.9, 61.0, 61.1, 61.2, 61.3, 61.4, 61.5, 61.6, 61.7, 61.8, 61.9, 62.0, 62.1, 62.2, 62.3, 62.4, 62.5, 62.6, 62.7, 62.8, 62.9, 63.0, 63.1, 63.2, 63.3, 63.4, 63.5, 63.6, 63.7, 63.8, 63.9, 64.0, 64.1, 64.2, 64.3, 64.4, 64.5, 64.6, 64.7, 64.8, 64.9, 65.0, 65.1, 65.2, 65.3, 65.4, 65.5, 65.6, 65.7, 65.8, 65.9, 66.0, 66.1, 66.2, 66.3, 66.4, 66.5, 66.6, 66.7, 66.8, 66.9, 67.0, 67.1, 67.2, 67.3, 67.4, 67.5, 67.6, 67.7, 67.8, 67.9, 68.0, 68.1

[illegible][illegible]

Age Group	1970	1980	1990	2000	2010	2020
0-14	25	22	18	15	12	10
15-24	20	18	15	12	10	8
25-34	15	14	13	12	11	10
35-44	12	11	10	9	8	7
45-54	10	9	8	7	6	5
55-64	8	7	6	5	4	3
65-74	15	18	22	25	28	35
75+	5	6	7	8	9	12

THE UNIVERSITY OF CHICAGO

[illegible][illegible]

**M**

1. *Method* : Willard  
 2. *Subject* : Mathematics  
 3. *Grade* : 10  
 4. *Teacher* : Mr. Smith

ATTORNEY AT LAW  
 1001  
 1001  
 1001

ADP: ATP RATIO: 1.0  
 PHOSPHATE: 0.1  
 AMINO ACIDS: 0.001 PMAN: 0.001

PROLIFERATION OF *STREPTOCOCCUS* IN THE  
PERITONEAL CAVITY OF MICE WITH  
PERITONITIS CAUSED BY *STREPTOCOCCUS*  
FELICIS VARIANTS AND *STREPTOCOCCUS*  $\alpha$ -

THEORY:  $\sigma = \frac{F}{A}$  and  $\epsilon = \frac{\Delta L}{L}$

[illegible][illegible][illegible]

Figure 1. Schematic representation of the experimental design. The subjects were divided into two groups: a control group (C) and an experimental group (E). The control group received a placebo (P) and the experimental group received a treatment (T). The subjects were divided into two groups: a control group (C) and an experimental group (E). The control group received a placebo (P) and the experimental group received a treatment (T). The subjects were divided into two groups: a control group (C) and an experimental group (E). The control group received a placebo (P) and the experimental group received a treatment (T).

## GENERAL INFORMATION

[illegible]

100

**MULTIPLYING THE EFFECTS OF THE MONTAGNA**  
The Montagna is a small, rugged mountain in the heart of the Italian Alps. It is a place of great beauty and tranquility, with its steep slopes and dense forests. The Montagna is a place where the effects of the environment are multiplied, and the effects of the human presence are minimized. The Montagna is a place where the effects of the environment are multiplied, and the effects of the human presence are minimized.

[illegible][illegible]

NAME: Robert N. Meyer  
 ADDRESS: 1000 17th St. N.W.  
Washington, D.C. 20036  
 PHONE: 202-331-1100

1. The first step is to identify the problem or question that needs to be addressed. This involves understanding the context and the specific requirements of the task.

Figure 1. The effect of the number of trials on the number of correct responses. The number of correct responses was significantly higher for the 10 trials condition than for the 5 trials condition. Error bars represent the standard error of the mean.

[illegible][illegible]

the 1990s, the number of people in the world who are under 15 years of age is expected to increase from 1.1 billion to 1.5 billion. The number of people aged 65 and over is expected to increase from 200 million to 400 million. The number of people aged 15 and over is expected to increase from 3.5 billion to 4.5 billion. The number of people aged 15 and over is expected to increase from 3.5 billion to 4.5 billion. The number of people aged 15 and over is expected to increase from 3.5 billion to 4.5 billion.

**Author's Address:** Department of Psychology,  
University of Illinois at Chicago, Chicago, IL  
60607-7181.  
E-mail: jay@uic.edu

Figure 1. The effect of the concentration of the *Agrobacterium* suspension on the transformation efficiency of *Agrobacterium* strains. The concentration of the *Agrobacterium* suspension was 10<sup>6</sup> cells/ml (○), 10<sup>7</sup> cells/ml (□), 10<sup>8</sup> cells/ml (△), and 10<sup>9</sup> cells/ml (◇). The error bars represent the standard deviation of three independent experiments.

Med. M. with Faculty of Medicine, University of Medicine and Pharmacy, Bucharest, Romania

1. The above information is true and correct to the best of my knowledge and belief.

1. *Amphiprion melanopus* (Forsk.)  
 2. *A. melanopus* (Forsk.)  
 3. *A. melanopus* (Forsk.)  
 4. *A. melanopus* (Forsk.)  
 5. *A. melanopus* (Forsk.)  
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 97. *A. melanopus* (Forsk.)  
 98. *A. melanopus* (Forsk.)  
 99. *A. melanopus* (Forsk.)  
 100. *A. melanopus* (Forsk.)

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-887-0400  
TELEFAX: 202-887-0605  
TELEX: 440864

INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids

TYPE: AMINO ACID  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
HYPOTHETICAL: YES

US-07-776-272-25

Query Match: 48.9% Score: 104.5, E-11, Length: 26,  
Best Local Similarity: 44.4% (Pctd No. 1,26,007)

Matches: 24; Conservative: 1; Mismatches: 1; Indels: 1; Gaps: 1

QY 1 HSDGFTSELSPEPCAPLPGV 27  
|||||  
DB 1 HSDGFTSELSPEPCAPLPGV 27

PLT 12  
US-09-303-799D-26

Sequence 26, Application US/09303799D  
Patent No. 6380357

GENERAL INFORMATION:  
APPLICANT: Hoffmann, Ronald

APPLICANT: Hoffmann, James

FILE REFERENCE: X-10242  
TITLE OF INVENTION: GLOMADIN-LIKE PEPTIDE-1 CRYSTALS

CURRENT APPLICATION NUMBER: US/09303799D  
CURRENT FILING DATE: 1999-12-11

NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn version 3.0

SEQ ID NO: 26

LENGTH: 31

TYPE: PPT

ORGANISM: Artificial

FEATURE: OTHER INFORMATION: synthetic construct

US-09-209-799D-26

Query Match: 47.3% Score: 82.15, E-11, Length: 31,  
Best Local Similarity: 44.4% (Pctd No. 1,26,007)

Matches: 12; Conservative: 4; Mismatches: 9; Indels: 0; Gaps: 0

QY 1 HSDGFTSELSPEPCAPLPGV 31  
|||||  
DB 1 HSDGFTSELSPEPCAPLPGV 31

RESULT 13

US-09-302-596-11  
Sequence 11, Application US/0930259611

Patent No. 6294722

GENERAL INFORMATION:  
APPLICANT: Ehlert, Thomas E.

APPLICANT: Ehlert, Mario R W.

TITLE OF INVENTION: Methods and compositions for the detection of  
TITLE OF INVENTION: 15-hydroxy and 16-hydroxy tissue

FILE REFERENCE: P03660051  
CURRENT APPLICATION NUMBER: US/09302596

CURRENT FILING DATE: 1999-04-13  
PRIOR APPLICATION NUMBER: 60/103,493

PRIOR FILING DATE: 1999-10-06  
NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 11

LENGTH: 37

TYPE: PPT

ORGANISM: Gila monster venom

US-09-302-596-11

Query Match: 46.3% Score: 61.0, E-11, DB: 4, Length: 37,  
Best Local Similarity: 44.4% (Pctd No. 2,017)

Matches: 12; Conservative: 0; Mismatches: 9; Indels: 0; Gaps: 0

QY 1 HSDGFTSELSPEPCAPLPGV 27  
|||||  
DB 1 HSDGFTSELSPEPCAPLPGV 27

RESULT 14

US-09-333-415-11  
Sequence 11, Application US/0933341511

Patent No. 634180

GENERAL INFORMATION:  
APPLICANT: Holst, Jens O.

APPLICANT: Valicoll, Tina  
TITLE OF INVENTION: GDF-1 as a Diagnostic Test to Determine Post-Test

TITLE OF INVENTION: Evaluation and Use of Diagnostic Test to Determine Post-Test

FILE REFERENCE: P03960050  
CURRENT APPLICATION NUMBER: US/0933341511

CURRENT FILING DATE: 1999-06-03  
NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 11

LENGTH: 37

TYPE: PPT

ORGANISM: Helicoverpa suspensa

US-09-333-415-11

Query Match: 46.3% Score: 61.0, E-11, DB: 4, Length: 37,  
Best Local Similarity: 44.4% (Pctd No. 2,017)

Matches: 12; Conservative: 0; Mismatches: 9; Indels: 0; Gaps: 0

QY 1 HSDGFTSELSPEPCAPLPGV 17  
|||||  
DB 1 HSDGFTSELSPEPCAPLPGV 17

RESULT 15

US-09-303-016-11  
Sequence 11, Application US/0930301611

Patent No. 632197

GENERAL INFORMATION:  
APPLICANT: Ehlert, Thomas E.

APPLICANT: Ehlert, Mario R W.

TITLE OF INVENTION: Methods and compositions for the detection of  
TITLE OF INVENTION: Active Analgesics in Tissue the presence of the

FILE REFERENCE: P03660052  
CURRENT APPLICATION NUMBER: US/0930301611

CURRENT FILING DATE: 1999-04-13  
PRIOR APPLICATION NUMBER: 60/103,493

PRIOR FILING DATE: 1999-10-06  
NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 11

LENGTH: 37

TYPE: PPT

ORGANISM: Helicoverpa suspensa

US-09-303-016-11

Query Match: 46.3% Score: 61.0, E-11, DB: 4, Length: 37,  
Best Local Similarity: 44.4% (Pctd No. 2,017)

Matches: 12; Conservative: 0; Mismatches: 9; Indels: 0; Gaps: 0

QY 1 HSDGFTSELSPEPCAPLPGV 27  
|||||  
DB 1 HSDGFTSELSPEPCAPLPGV 27

Tue May 27 13:06:14 2003

us-09-897-412-10.rai

Page 6

2003-05-27 13:06:14  
us-09-897-412-10.rai







US-09-847-249A-10  
Query Match  
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US-09-847-249A-10  
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Query Match  
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US-09-847-249A-10  
Query Match  
Best Local Similarity 93.2% Score 123 DB 10 Length 27  
Matches 25 Conservative 1 Mismatches 1 Indels 0 Gaps 0

26 HONORABLE SERVICE AGENCY  
27 HONORABLE SERVICE AGENCY

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89 HONORABLE SERVICE AGENCY

90 HONORABLE SERVICE AGENCY

US-09-847-249A-28  
; Sequence 28, Application US/68947249A  
; Publication No. US20030032588A1  
; GENERAL INFORMATION:  
; APPLICANT: MARSHALL, WILLIAM S.  
; APPLICANT: STARK, KEVIN LEE  
; TITLE OF INVENTION: GLUCAGON ANTAGONIST  
; FILE REFERENCE: A-693  
; CURRENT APPLICATION NUMBER: US/09/847,249A  
; CURRENT FILING DATE: 2001-05-02  
; PRIORITY APPLICATION NUMBER: 60/201,436  
; PRIORITY FILING DATE: 2000-05-03  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 28  
; LENGTH: 29  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Glucagon Antagonist  
; NAME/KEY: misc.feature  
; LOCATION: (21)..(21)  
; OTHER INFORMATION: Xaa is isoleucine (Ile)  
09-847-249A-28

Query Match 47.7%, Score 63, DB 3, Length 29,  
Best Local Similarity 48.1%, Pred. No. 0.01,  
Matches 13, Conservative 4, Mismatches 10, Indels 0, Gaps 0

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||| ||| : ||| :  
EQ 1 HSGGFTSELSRLEFQAPLQGLGV 27

Search completed: May 23, 2003, 09:04:09  
Job time: 17 secs



GenBank version 5.1.4 FS 4578  
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## OM protein - protein search, using sw model

Run on: May 27, 2003, 09:01:07, Search time: 16 seconds  
(without alignments)

162,000 Matches with alignment

Title: US-09-897-412-10

Perfect score: 132

Sequence: 1 HSDGFTESELRLESGARLQFLQSLV 27

Scoring table:

BLOSUM62

Gapop 10 0, Gapext 0.5

Searched: 282224 seqs, 36134400 residues

Total number of hits satisfying chosen parameters: 282224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match: 18

Maximum Match: 100%

Listing first 45 summaries

## Database:

1: p1r1:  
2: p1r2:  
3: p1r3:  
4: p1r4:

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	132	100.0	27	1 S07443	secretin - human
2	126	95.5	27	2 A07267	secretin - dog
3	123	93.2	27	1 S800	secretin - bovine
4	123	93.2	27	1 S800	secretin - bovine
5	123	93.2	27	1 S800	secretin - bovine
6	113	80.2	134	1 S800	secretin precursor
7	113	80.2	134	1 S800	secretin precursor
8	113	80.2	134	1 S800	secretin precursor
9	113	80.2	134	1 S800	secretin precursor
10	113	80.2	134	1 S800	secretin precursor
11	113	80.2	134	1 S800	secretin precursor
12	113	80.2	134	1 S800	secretin precursor
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14	113	80.2	134	1 S800	secretin precursor
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16	113	80.2	134	1 S800	secretin precursor
17	113	80.2	134	1 S800	secretin precursor
18	113	80.2	134	1 S800	secretin precursor
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27	113	80.2	134	1 S800	secretin precursor
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30	113	80.2	134	1 S800	secretin precursor

30	59	44.7	206	1	15131	secretin - human
31	59	43.9	29	1	6026	secretin - human
32	57	43.2	23	1	6026	secretin - human
33	57	43.2	23	1	6026	secretin - human
34	57	43.2	23	1	6026	secretin - human
35	57	43.2	23	1	6026	secretin - human
36	57	43.2	23	1	6026	secretin - human
37	57	43.2	23	1	6026	secretin - human
38	57	43.2	23	1	6026	secretin - human
39	57	43.2	23	1	6026	secretin - human
40	56	42.4	55	1	VRSH	secretin - human
41	56	42.4	170	1	VRSH	secretin - human
42	56	42.4	170	1	VRSH	secretin - human
43	56	42.4	170	1	VRSH	secretin - human
44	56	42.4	170	1	VRSH	secretin - human
45	56	42.4	170	1	VRSH	secretin - human

## ALIGNMENTS

## RESULT 1

S07443

secretin - human

CSpecies: Homo sapiens (man)

CDate: 1988-1990 Hs498994.1 (GenBank) #101 change 10/09/1999

CAccession: S07443

PCopyright: M. J. G. (1993), N. J. G. (1993), N. J. G. (1993), N. J. G. (1993)

IKOS Med. Sci. 13, 217-218, 1995

ATitle: Human secretin is not identical to the porcine/bovine secretin

AReference number: S07443

AAccession: S07443

AMolecule type: protein

AProtein type: protein

AProtein type: protein

AProtein type: protein

AProtein type: protein

AProtein type: protein

AProtein type: protein

AProtein type: protein

AProtein type: protein

AProtein type: protein

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Journal of Interpersonal Violence 26(1) 100-116  
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DOI: 10.1177/0886260510392094  
jiv.sagepub.com

[illegible][illegible][illegible]

**Figure 1**

The Modified Interpolated Method of Van der Pol was experimentally found to be more accurate than the other methods.

[illegible]

Figure 1. The effect of the concentration of the *Agrobacterium* suspension on the transformation efficiency of *Agrobacterium* strains. The *Agrobacterium* strains were grown in YEA medium for 24 h at 28 °C. The cell concentration of the strains was adjusted to 1.0 × 10<sup>8</sup> cells/ml. The cell suspension was then diluted to 10<sup>6</sup>, 10<sup>7</sup>, 10<sup>8</sup>, 10<sup>9</sup>, and 10<sup>10</sup> cells/ml. The cell suspension was then inoculated into the plant tissue. The transformation efficiency was determined by the number of transformants per 10<sup>6</sup> cells. The data were expressed as the mean ± SD of three independent experiments.

[illegible]

	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2433	2434	2435	2436	2437	2438	2439	2440	2441	2442	2
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1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650, 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658, 2659, 2660, 2661, 2662, 2663, 2664, 2665, 2666, 2667, 2668, 2669, 2670, 2671, 2672, 2673, 2674, 2675, 2676, 2677, 2678, 26

[illegible]

Figure 1 consists of 16 small, black-and-white micrographs arranged in a 4x4 grid. Each image shows a different stage or component of the life cycle of the parasitic flatworm. The images include:
 

- Eggs: Small, oval-shaped structures, some with distinct polar capsules.
- Larvae: Early developmental stages, some showing cilia or flagella.
- Adult worms: More complex, elongated structures, some showing internal organs or reproductive structures.
- Other stages: Some images show clusters of organisms or specific anatomical details.

1. The first step in the process is to identify the problem or issue that needs to be addressed. This involves gathering information and understanding the context of the problem.

*(continued)*

[illegible][illegible]

Figure 1 is a line graph showing the percentage of total energy expenditure (TEE) for different activities over a 24-hour period. The Y-axis is 'Percentage of TEE' (0-100) and the X-axis is 'Time of day' (0-24). The activities and their approximate percentages are:

Time of day	Sleeping	Resting	Sitting	Standing	Walking	Running
0	50	10	10	10	10	10
1	50	10	10	10	10	10
2	50	10	10	10	10	10
3	50	10	10	10	10	10
4	50	10	10	10	10	10
5	50	10	10	10	10	10
6	50	10	10	10	10	10
7	50	10	10	10	10	10
8	50	10	10	10	10	10
9	50	10	10	10	10	10
10	50	10	10	10	10	10
11	50	10	10	10	10	10
12	50	10	10	10	10	10
13	50	10	10	10	10	10
14	50	10	10	10	10	10
15	50	10	10	10	10	10
16	50	10	10	10	10	10
17	50	10	10	10	10	10
18	50	10	10	10	10	10
19	50	10	10	10	10	10
20	50	10	10	10	10	10
21	50	10	10	10	10	10
22	50	10	10	10	10	10
23	50	10	10	10	10	10
24	50	10	10	10	10	10

[illegible][illegible][illegible]

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1. The first step is to identify the problem or question that needs to be addressed. This involves understanding the context and the specific requirements of the task.







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Best Local Similarity 44.4%; Pred No 0.019;  
Matches 12; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 HSDGFTSELSPFPGAPLQPLQSLV 27  
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